

RESULT 5  
 AAW97357  
 ID AAW97357 standard; peptide; 574 AA.  
 XX  
 AC AAW97357;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE Protein sequence of the specification.  
 XX  
 KW Retrovirus; gene transfer; serum-free medium; AIDS; cancer; leukaemia;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9905301-A1.  
 XX  
 PD 04-FEB-1999.  
 XX  
 PF 15-JUL-1998; 98WO-JP003173.  
 XX  
 PR 23-JUL-1997; 97JP-00196772.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 PI Bagnis C, Imbert A, Mannoni P;  
 XX  
 DR WPI; 1999-142951/12.  
 XX  
 PT Gene transfer by retrovirus in medium containing functional substance and  
 PT optionally low-density lipoprotein - useful in medical sciences, cell and  
 PT gene engineering, particularly for treating AIDS and cancers.  
 XX  
 PS Claim 5; Page 27-30; 32pp; Japanese.  
 XX  
 CC The specification describes a method for transferring a gene into target  
 CC cells by a retrovirus using a serum-free medium. The culture medium of  
 CC the target cells is serum free and contains an effective amount of a  
 CC functional substance to elevate the gene transfer efficiency when both  
 CC the retrovirus and target cells are present together. The gene transfer  
 CC method is useful in medical sciences, cell engineering and genetic  
 CC engineering, such as in the treatment of AIDS and cancers e.g. leukaemia  
 CC by gene therapy  
 XX  
 SQ Sequence 574 AA;  
  
 Query Match 100.0%; Score 2968; DB 1; Length 574;  
 Best Local Similarity 100.0%;  
 Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	PTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSI	SPSDNAVVLTNLL	60
Db	1	PTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSI	SPSDNAVVLTNLL	60
Qy	61	PGTEYVVSVSVEQHESTPLRGROKTGLDSPTGIDFSDITANSFTVH	WIAPRATITGYR	120
Db	61	PGTEYVVSVSVEQHESTPLRGROKTGLDSPTGIDFSDITANSFTVH	WIAPRATITGYR	120
Qy	121	IRHHPEHFSGRPREDRVPHSRNSITLTNLTGTEYVVSIVALNGREES	PLLIQQSTVSD	180
Db	121	IRHHPEHFSGRPREDRVPHSRNSITLTNLTGTEYVVSIVALNGREES	PLLIQQSTVSD	180
Qy	181	VPRDLEVVAATPTSLLSWDAPAVTVRYYRITYGETGGNSPVQEF	TVPGSKSTATISGLK	240
Db	181	VPRDLEVVAATPTSLLSWDAPAVTVRYYRITYGETGGNSPVQEF	TVPGSKSTATISGLK	240
Qy	241	PGVDYITITVYAVTGRGDSPASSKPISINRYTEIDKPSMAIPAP	TDLKFTQVTPITSLAQW	300
Db	241	PGVDYITITVYAVTGRGDSPASSKPISINRYTEIDKPSMAIPAP	TDLKFTQVTPITSLAQW	300
Qy	301	TPPNVQLTGYYRVVTPKEKTGPMKEINLAPDSSSVVSGLMVATK	YEVSVYALKDTLTSR	360
Db	301	TPPNVQLTGYYRVVTPKEKTGPMKEINLAPDSSSVVSGLMVATK	YEVSVYALKDTLTSR	360
Qy	361	PAQGVVTTLENVSPRRARVTDATETTTITISWRTKTETITGFQV	DAVPANGQTPIQRTIK	420
Db	361	PAQGVVTTLENVSPRRARVTDATETTTITISWRTKTETITGFQV	DAVPANGQTPIQRTIK	420
Qy	421	PDVRSYTTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAID	APSNLRFATTNPNSLLVS	480
Db	421	PDVRSYTTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAID	APSNLRFATTNPNSLLVS	480
Qy	481	WQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEP	GTETIYVIALKNNQKS	540
Db	481	WQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEP	GTETIYVIALKNNQKS	540
Qy	541	EPLIGRKKTDLPQLVLTLPHPNLHGFEILDVPST	574	
Db	541	EPLIGRKKTDLPQLVLTLPHPNLHGFEILDVPST	574	